```
  1 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
    CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG

101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CCATGGCCCG
    GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC
  1                                                                                                   MetAlaArg

201 GATCCCCAAG ACCCTAAAGT TCGTCGTCGT CATCGTCGCG GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
    CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC
  4  IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln

301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
    GTCTGTCACC GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCAC AGGTCGTCCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
 37 GlnThrValA laProGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
    GTCTCCCACA CCTAATGTGG TTGCGAAGGT TGTTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA
 71   GluGlyVa lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
    CTGGTCTCTG TGTCACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCCTTCAG
104  ThrArgAsp ThrValCysG lnCysLysGl uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSerA rgCysProSe rGlyGluVal

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAACA
    GTTCAGTCAT TAACATGCAG GACCCTACTA TAGGTCACAC AACTTCTTAA ACCACGGTTA CGGTGACACC TTTGGGGTCG ACGACTTCTC TGTTACTTGT
137 GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG
    GGTCGGGCCC CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTTGTGGTCG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC
171   SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly
```

FIG._1A-1

```
 801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCCTGCC
     CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTGGTGGTCG GGCCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC CTGAGGACGG
 204  ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla

 901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTT GAAAGACTTC ACTGTGGAAG AAATTCCTTC
     AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAACA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG
 237 SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal

1001 CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCT
     GAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCCGCGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA

1101 GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
     CGGGGACGGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT
```

FIG._1A-2

```
   1 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
     CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG
                                                                                    MetGlnGl yValLysGlu ArgPheLeuPro
 -40

 101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CCATGGCCCG
     GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC
 -30   LeuGlyAs nSerGlyAsp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHisT hrMetAlaArg

 201 GATCCCCAAG ACCCTAAAGT TCGTCGTCGT CATCGTCGCG GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
     CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC
   4  IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln

 301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
     GTCTGTCACC GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCAC AGGTCGTCCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
  37 GlnThrValA laProGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr
```

FIG._1B-1

```
401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
    GTCTCCCACA CCTAATGTGG TTGCGAAGGT TGTTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA
 71   GluGlyVa lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
    CTGGTCTCTG TGTCACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCCTTCAG
104  ThrArgAsp ThrValCysG lnCysLysGl uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSerA rgCysProSe rGlyGluVal

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAACA
    GTTCAGTCAT TAACATGCAG GACCCTACTA TAGGTCACAC AACTTCTTAA ACCACGGTTA CGGTGACACC TTTGGGGTCG ACGACTTCTC TGTTACTTGT
137 GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG
    GGTCGGGCCC CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTTGTGGTCG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC
171   SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly

801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCCTGCC
    CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTGGTGGTCG GGCCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC CTGAGGACGG
204  ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla

901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTT GAAAGACTTC ACTGTGGAAG AAATTCCTTC
    AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAACA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG
237 SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal

1001 CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCT
     GAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCCGCGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA

1101 GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
     CGGGGACGGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT
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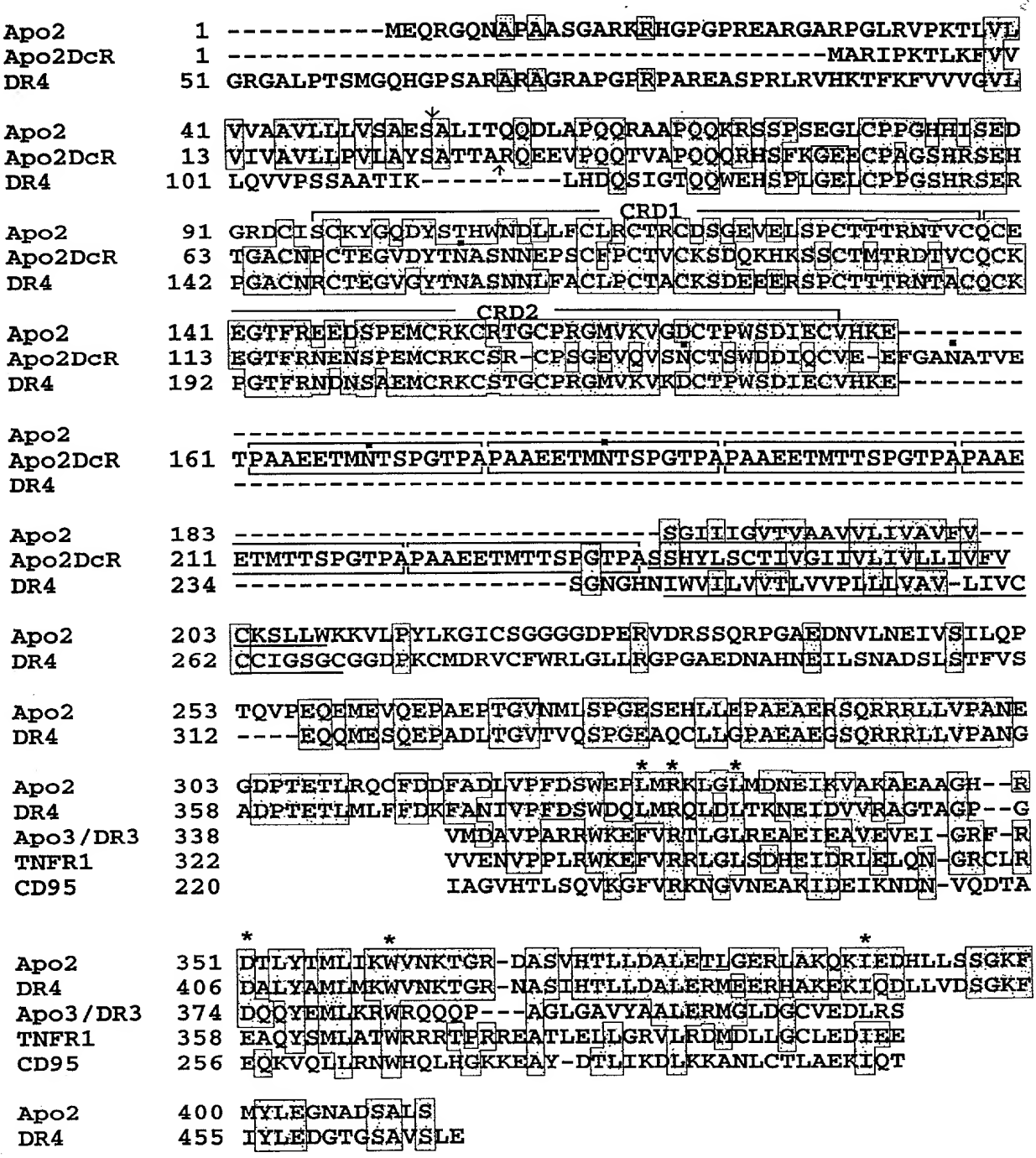
FIG._1B-2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Apo2DcR 1 ----------MARIPKTLKFVV
DR4 51 GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFVVVGVL
Apo2 41 VVAAVLLLVSAESALITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISED
Apo2DcR 13 VIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH
DR4 101 LQVVPSSAATIK----------LHDQSIGTQQWEHSPLGELCPPGSHRSER
CRD1
Apo2 91 GRDCISCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCE
Apo2DcR 63 TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCK
DR4 142 PGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCK
CRD2
Apo2 141 EGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVHKE----------
Apo2DcR 113 EGTFRNENSPEMCRKCSR-CPSGEVQVSNCTSWDDIQCVE-EFGANATVE
DR4 192 PGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSDIECVHKE--------
Apo2 ----------
Apo2DcR 161 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4 ----------
Apo2 183 ----------SGIIIGVTVAAVVLIVAVFV---
Apo2DcR 211 ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4 234 ----------SGNGHNIWVILVVTLVVPLLLVAV-LIVC
Apo2 203 CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4 262 CCIGSGCGGDPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2 253 TQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPANE
DR4 312 ----EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLLVPANG
Apo2 303 GDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGH--R
DR4 358 ADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTAGP--G
Apo3/DR3 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1 322 VVENVPPLRWKEFVRRLGLSDHEIDRLELQN-GRCLR
CD95 220 IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN-VQDTA
Apo2 351 DTLYIMLIKWVNKTGR-DASVHTLLDALETLGERLAKQKIEDHLLSSGKF
DR4 406 DALYAMLMKWVNKTGR-NASIHTLLDALERMEERHAKEKIQDLLVDSGKF
Apo3/DR3 374 DQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1 358 EAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEE
CD95 256 EQKVQLLRNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT
Apo2 400 MYLEGNADSALS
DR4 455 IYLEDGTGSAVSLE

FIG._2

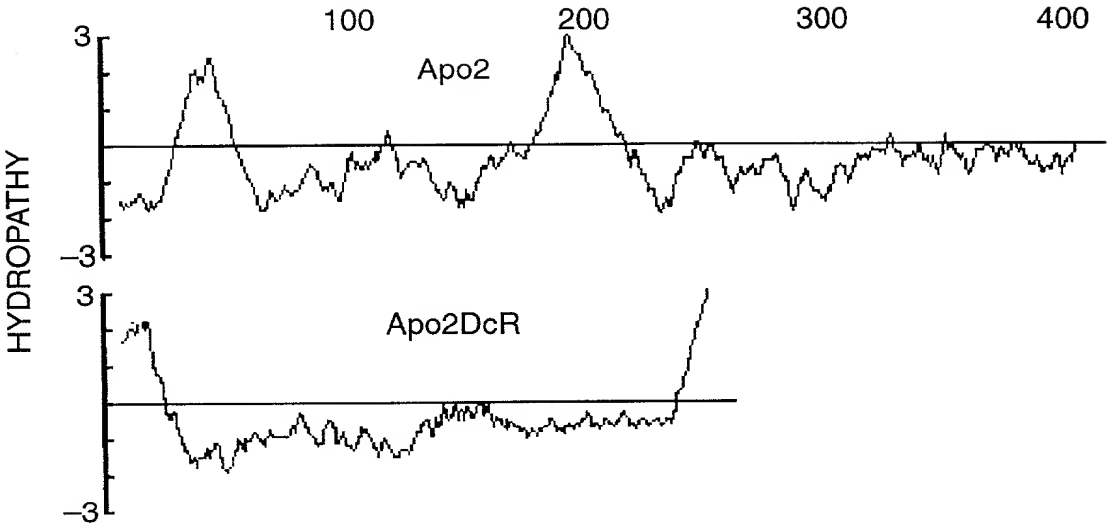


FIG._3

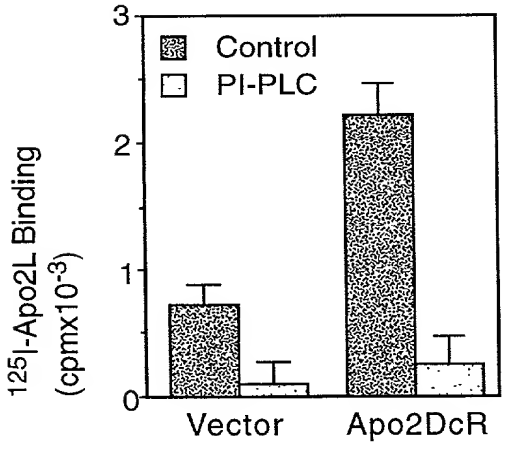


FIG._4

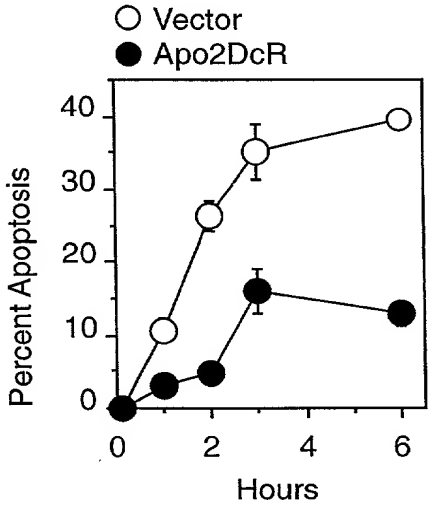
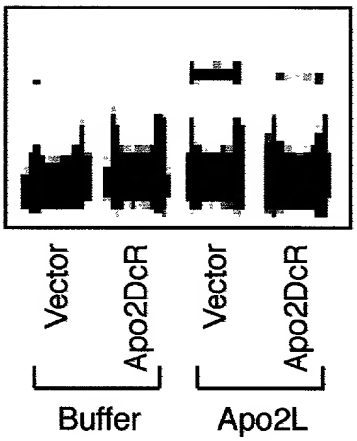


FIG._5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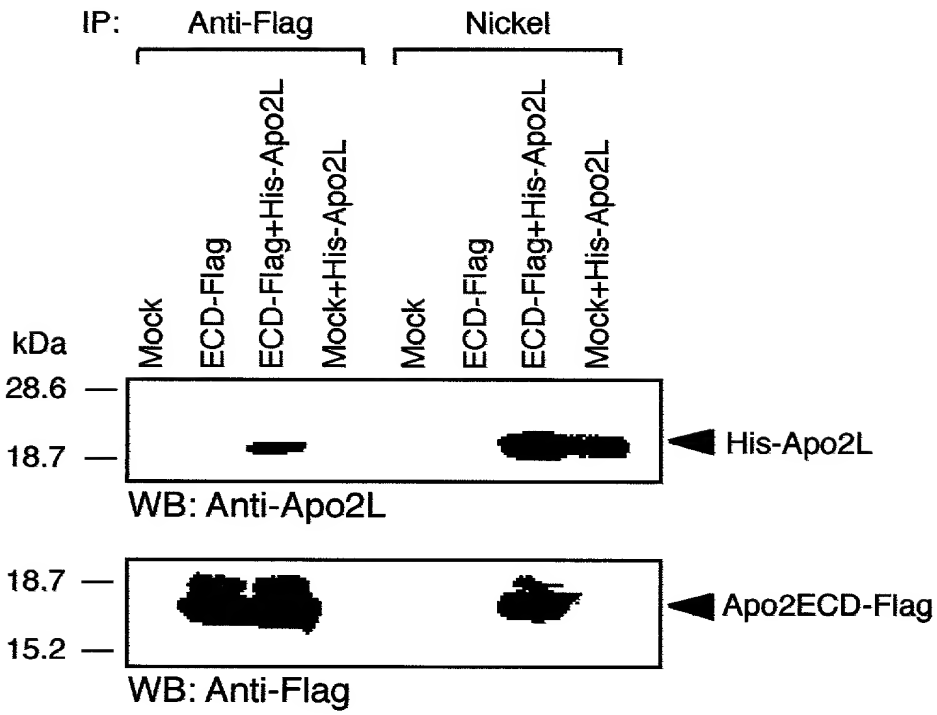
Vector
Apo2DcR
Buffer
Apo2L

FIG._6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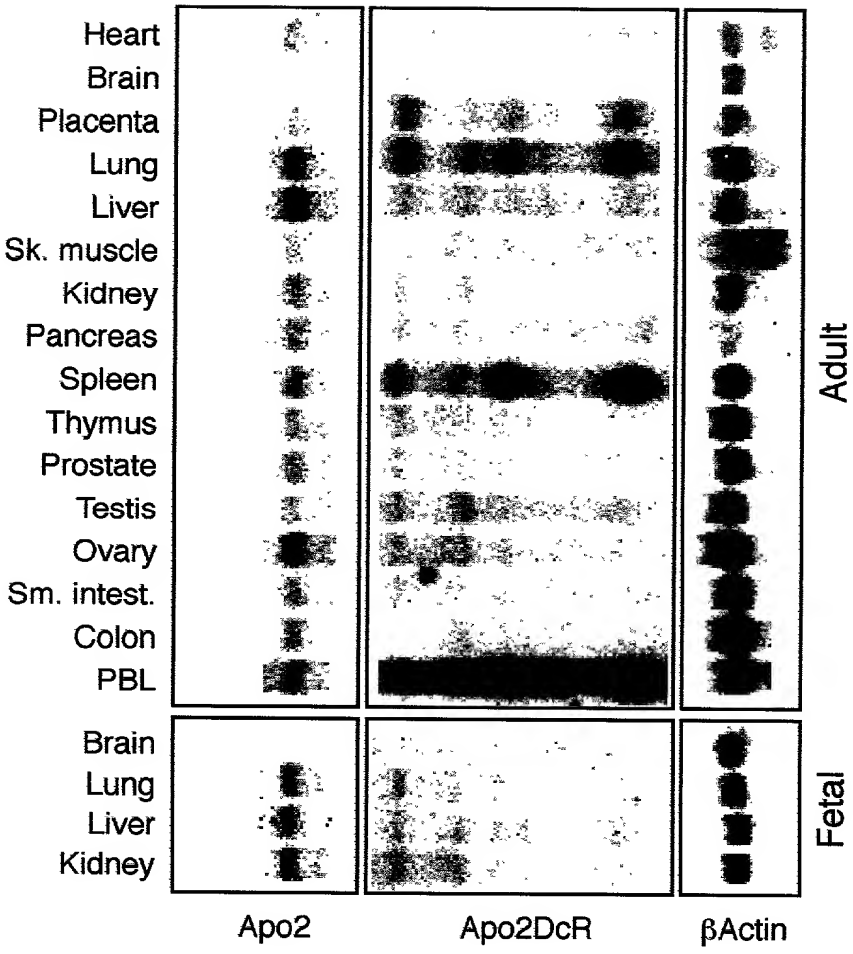
Nickel
Mock
ECD-Flag
ECD-Flag+His-Apo2L
Mock+His-Apo2L
Mock
ECD-Flag
ECD-Flag+His-Apo2L
Mock+His-Apo2L
kDa
28.6
18.7
His-Apo2L
WB: Anti-Apo2L
18.7
15.2
Apo2ECD-Flag
WB: Anti-Flag

FIG._10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Brain
Placenta
Lung
Liver
Sk. muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Ovary
Sm. intest.
Colon
PBL
Brain
Lung
Liver
Kidney
Adult
Fetal
Apo2
Apo2DcR
βActin

FIG._7

```
  1 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC
    GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG

101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC CCGGAAAAGG CACGGCCCAG
    GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC
  1                                          M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGGA GGCGCGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGC
    CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC GACTCAGACG
 22   ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCCACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
    AGACTAGTGG GTTGTTCTGG ATCGAGGGGT CGTCTCTCGC CGGGGTGTTG TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG
 55  LeuIleThr GlnGlnAspL euAlaProGl nGlnArgAla AlaProGlnG lnLysArgSe rSerProSer GluGlyLeuC ysProProGl yHisHisIle

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
    AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CGCGACGTGG TCCACACTAA
 88 SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG
    GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC
122   GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg

601 GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA
    CTTCACGGCG TGTCCCACAG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
155  LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIleIle

701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAGAAAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG
    CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly
```

FIG._8A-1

```
 801 GTGGTGGTGG GGACCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCCACCCA
     CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
 222   GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln

 901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
     CCAGGGACTC GTCCTTTACC TTCAGGTCCT CGGTCGTCTC GGTTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
 255  ValProGlu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuGl uProAlaGlu

1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC
     CGACTTTCCA GAGTCTCCTC CTCCGACGAC CAAGGTCGTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro
```

FIG._8A-2

```
1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA
     GGAAACTGAG GACCCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTCC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC TGTGGAACAT
 322   PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr

1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
     GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
 355  ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln

1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
     TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXqqS erOC*

1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
     GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG

1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT
     GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTCG ACTTACACTA TTATTCCTGT GATACCTTTA

1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
     CAGACCTAGT AAGGCAAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA

1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
     AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTC CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG
```

FIG._8B

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  1 MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESALITQQD
 61 LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCLRCTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVH
181 KESGIIIGVTVAAVVLIVAVFVCKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAED
241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPA
301 NEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKW
361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS
```

FIG._9

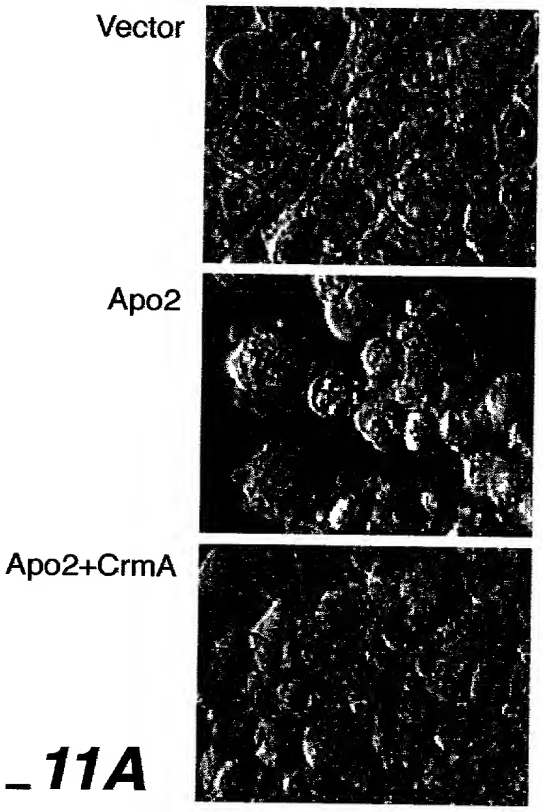

FIG._11A

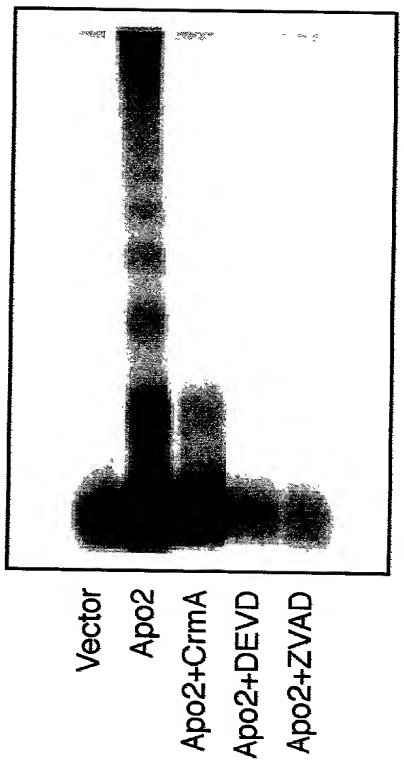

FIG._11B

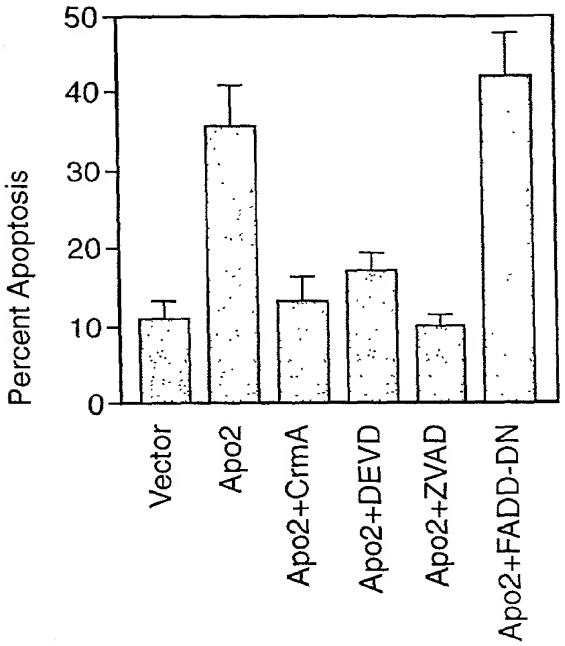

FIG._11C

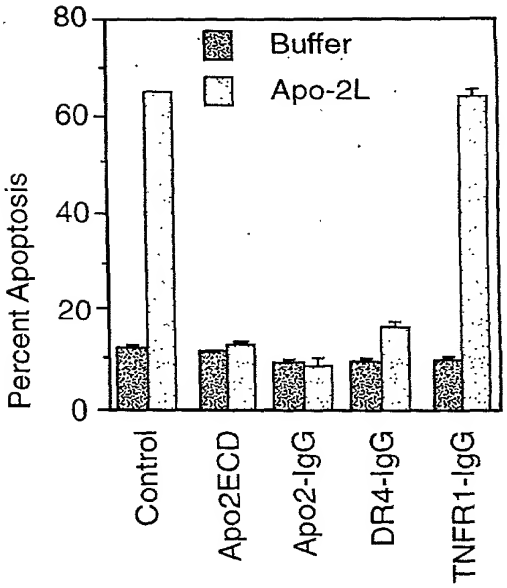

FIG._11D

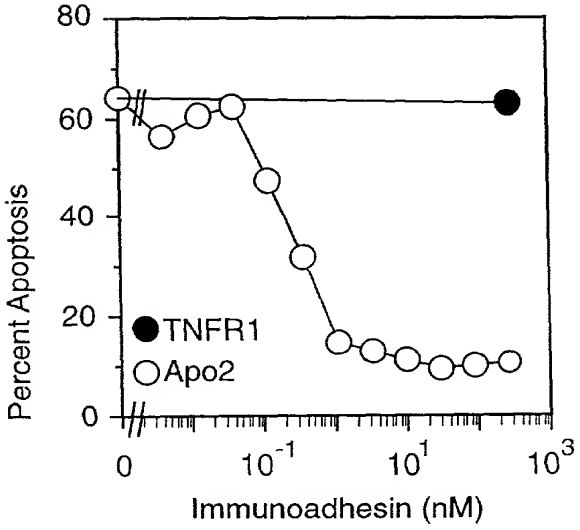

FIG._11E

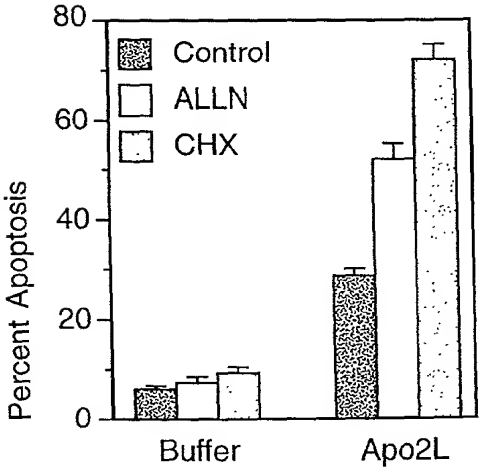

FIG._12C

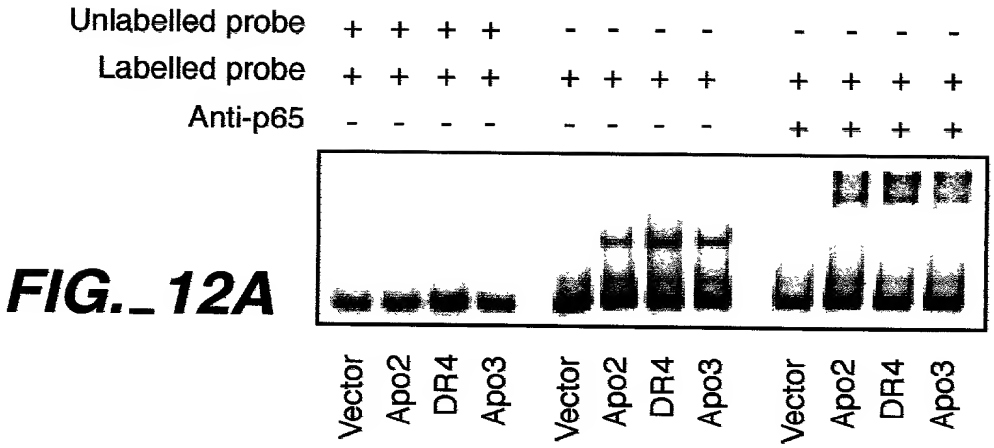

FIG._12A

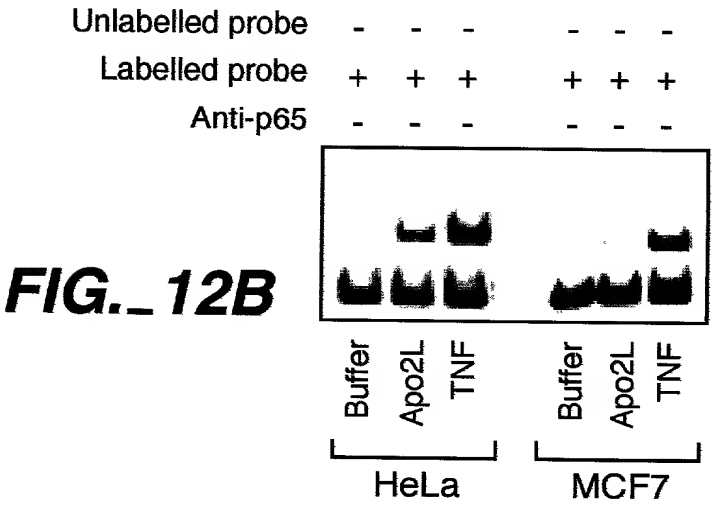

FIG._12B

FIG._13